

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 12:20:40 ; Search time 1692 Seconds
(without alignments)
764.885 Million cell updates/sec

Title: US-10-089-380-5

Perfect score: 34

Sequence: 1 gaagttctactttctgagaatgaacttc 34

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: gb_est1.*

2: gb_est2.*

3: gb_est3.*

4: gb_est4.*

5: gb_est5.*

6: gb_est6.*

7: gb_est7.*

8: gb_est8.*

9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	32.4	95.3	74	9	CG654127
C 2	32.4	95.3	81	1	AI265023
C 3	32.4	95.3	81	1	AI265111
C 4	32.4	95.3	81	1	AI272501
C 5	32.4	95.3	88	1	AI316311
C 6	32.4	95.3	105	9	CG548652
C 7	32.4	95.3	112	9	CG606396
C 8	32.4	95.3	124	9	CG529627
C 9	32.4	95.3	130	9	CG529637
C 10	32.4	95.3	133	9	CG529602
C 11	32.4	95.3	135	9	CG529607
C 12	32.4	95.3	139	9	CG495088
C 13	32.4	95.3	140	9	CG667250
C 14	32.4	95.3	146	9	CG589974
C 15	32.4	95.3	151	9	CG666807
C 16	32.4	95.3	153	9	CG523992
C 17	32.4	95.3	161	9	CG609937
C 18	32.4	95.3	162	9	CG536645
C 19	32.4	95.3	168	9	CG529685
C 20	32.4	95.3	175	9	CR202574
C 21	32.4	95.3	182	9	CG522772
C 22	32.4	95.3	182	9	CG526410
C 23	32.4	95.3	189	9	CG528753
C 24	32.4	95.3	194	9	CG671483

C 25	32.4	95.3	206	9	CG668768
C 26	32.4	95.3	208	9	CR069250
C 27	32.4	95.3	216	9	CG573772
C 28	32.4	95.3	216	9	CG579328
C 29	32.4	95.3	219	9	CG667178
C 30	32.4	95.3	222	9	CR271082
C 31	32.4	95.3	228	9	CG669744
C 32	32.4	95.3	239	9	CG667464
C 33	32.4	95.3	241	9	CG670326
C 34	32.4	95.3	253	9	CG527478
C 35	32.4	95.3	254	9	CG667921
C 36	32.4	95.3	279	9	CG670404
C 37	32.4	95.3	280	9	CG545746
C 38	32.4	95.3	281	9	CG667916
C 39	32.4	95.3	285	9	CG666517
C 40	32.4	95.3	285	9	CG666761
C 41	32.4	95.3	293	9	CG666889
C 42	32.4	95.3	306	9	CG666905
C 43	32.4	95.3	314	9	CG557567
C 44	32.4	95.3	314	9	CG668319
C 45	32.4	95.3	316	9	CG667495

ALIGNMENTS

RESULT 1
CG654127/c

LOCUS

DEFINITION

CG654127

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

ORIGIN

Query Match

Best Local Similarity

Matches

33; Conservative

0; Mismatches

1; Indels

0; Gaps

0; Length 74;

Pred. No. 0.0086;

1; Indels

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Pred. No. 0.0086;

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Pred. No. 0.0086;

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Pred. No. 0.0086;

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1; Indels

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Pred. No. 0.0086;

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Pred. No. 0.0086;

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Pred. No. 0.0086;

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Pred. No. 0.0086;

1; Indels

0; Gaps

0; Length 74;

Pred. No. 0.0086;

1; Indels

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 15:17:50 ; Search time 306.75 Seconds
(without alignments)
718.497 Million cell updates/sec

Title: US-10-089-380-5

Perfect score: 34

Sequence: 1 gaggtctactattcttgagaaggaacttc 34

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	32.4	95.3	34	8	US-08-866-279A-14
C 2	32.4	95.3	34	9	US-09-920-932-2
C 3	32.4	95.3	34	9	US-09-804-653-7
C 4	32.4	95.3	34	9	US-09-748-739A-24
C 5	32.4	95.3	34	9	US-09-822-634-18
C 6	32.4	95.3	34	10	US-09-948-193-5
C 7	32.4	95.3	34	10	US-09-997-209-90
C 1	32.4	95.3	34	8	Sequence 14, Appl
C 2	32.4	95.3	34	9	Sequence 2, Appl
C 3	32.4	95.3	34	9	Sequence 7, Appl
C 4	32.4	95.3	34	9	Sequence 24, Appl
C 5	32.4	95.3	34	9	Sequence 18, Appl
C 6	32.4	95.3	34	10	Sequence 5, Appl
C 7	32.4	95.3	34	10	Sequence 90, Appl

RESULT 1

US-08-866-279A-14/c
; Sequence 14, Application US/08866279A
; Publication No. US20020170076A1
; GENERAL INFORMATION:
; APPLICANT: Susan DYMECKI
; TITLE OF INVENTION: Use of Flp Recombinase in Mice
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/866,279A
; FILING DATE: 30-MAY-1997
; CLASSIFICATION: 800
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

ALIGNMENTS

34	13	US-10-086-542A-3	Sequence 3, Appl
34	15	US-10-005-602-5	Sequence 5, Appl
34	15	US-10-353-445-10	Sequence 10, Appl
34	16	US-10-368-442-7	Sequence 7, Appl
34	17	US-10-430-907-1	Sequence 1, Appl
34	17	US-10-430-908-1	Sequence 1, Appl
34	17	US-10-440-030-1	Sequence 1, Appl
34	17	US-10-378-064-4	Sequence 4, Appl
34	17	US-10-444-664-3	Sequence 3, Appl
34	18	US-10-639-751-1	Sequence 1, Appl
34	18	US-10-433-206-90	Sequence 90, Appl
34	19	US-10-849-547-19	Sequence 19, Appl
34	20	US-10-623-386-18	Sequence 18, Appl
34	20	US-10-846-700-14	Sequence 14, Appl
34	21	US-10-469-508-44	Sequence 44, Appl
34	21	US-10-976-042-39	Sequence 39, Appl
34	22	US-10-954-721-18	Sequence 18, Appl
42	10	US-09-843-150-24	Sequence 24, Appl
42	10	US-09-843-150-25	Sequence 25, Appl
42	18	US-10-270-176-55	Sequence 55, Appl
42	20	US-10-475-962-24	Sequence 24, Appl
42	20	US-10-475-962-25	Sequence 25, Appl
48	8	US-08-866-279A-15	Sequence 15, Appl
48	9	US-09-351-819-2	Sequence 2, Appl
48	15	US-10-206-163-2	Sequence 2, Appl
48	15	US-10-161-403-62	Sequence 62, Appl
48	15	US-10-161-403-63	Sequence 63, Appl
48	16	US-10-252-279-3	Sequence 3, Appl
48	20	US-10-846-700-15	Sequence 15, Appl
54	8	US-08-866-279A-3	Sequence 3, Appl
54	20	US-10-846-700-3	Sequence 3, Appl
58	10	US-09-843-150-32	Sequence 32, Appl
58	10	US-09-843-150-33	Sequence 33, Appl
58	16	US-10-182-616-29	Sequence 29, Appl
58	16	US-10-182-616-30	Sequence 30, Appl
58	20	US-10-475-962-32	Sequence 32, Appl
58	20	US-10-475-962-33	Sequence 33, Appl
59	8	US-08-866-279A-2	Sequence 2, Appl

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 13:28:42 ; Search time 59.5 Seconds
(without alignments)
935.015 Million cell updates/sec

Title: US-10-089-380-5
Perfect score: 34
Sequence: 1 gaagttctatcttctggagaataggaaattc 34

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	32.4	95.3	34	1	US-08-484-324-3
C 2	32.4	95.3	34	1	US-08-486-409-3
C 3	32.4	95.3	34	2	US-08-864-224-18
C 4	32.4	95.3	34	2	US-08-975-763-3
C 5	32.4	95.3	34	2	US-08-825-784-3
C 6	32.4	95.3	34	2	US-08-972-258-4
C 7	32.4	95.3	34	3	US-09-011-257-2
C 8	32.4	95.3	34	3	US-08-745-404-5
C 9	32.4	95.3	34	3	US-09-263-128-4
C 10	32.4	95.3	34	3	US-09-193-502-1
C 11	32.4	95.3	34	3	US-09-193-503B-10
C 12	32.4	95.3	34	3	US-09-193-475-3
C 13	32.4	95.3	34	3	US-09-193-484-1
C 14	32.4	95.3	34	3	US-09-563-239-2
C 15	32.4	95.3	34	3	US-09-438-874A-1
C 16	32.4	95.3	34	3	US-09-439-158-1
C 17	32.4	95.3	34	4	US-09-415-839-10
C 18	32.4	95.3	34	4	US-09-718-034-1
C 19	32.4	95.3	34	4	US-09-606-323C-4
C 20	32.4	95.3	34	4	US-09-438-239-1
C 21	32.4	95.3	34	4	US-09-439-042A-1
C 22	32.4	95.3	34	4	US-09-455-050A-1
C 23	32.4	95.3	34	4	US-09-411-828-3
C 24	32.4	95.3	34	4	US-09-793-372-19
C 25	32.4	95.3	34	4	US-09-641-111A-4
C 26	32.4	95.3	34	4	US-09-869-185B-1
C 27	32.4	95.3	34	4	US-09-937-837-8

C 28	32.4	95.3	34	4	US-08-866-279A-14	Sequence 14, Appl
C 29	32.4	95.3	34	4	US-09-122-384-18	Sequence 18, Appl
C 30	32.4	95.3	34	5	PCT-US92-01899-3	Sequence 3, Appl
C 31	32.4	95.3	36	4	US-09-869-185B-14	Sequence 11, Appl
C 32	32.4	95.3	40	4	US-09-869-185B-11	Sequence 14, Appl
C 33	32.4	95.3	40	4	US-09-869-185B-12	Sequence 12, Appl
C 34	32.4	95.3	44	4	US-09-869-185B-13	Sequence 13, Appl
C 35	32.4	95.3	48	4	US-08-866-279A-15	Sequence 15, Appl
C 36	32.4	95.3	51	3	US-09-837-863-3	Sequence 3, Appl
C 37	32.4	95.3	51	3	US-09-837-863-4	Sequence 4, Appl
C 38	32.4	95.3	52	3	US-09-837-863-11	Sequence 11, Appl
C 39	32.4	95.3	52	3	US-09-837-863-12	Sequence 12, Appl
C 40	32.4	95.3	53	3	US-09-837-863-5	Sequence 5, Appl
C 41	32.4	95.3	53	3	US-09-837-863-6	Sequence 6, Appl
C 42	32.4	95.3	54	1	US-08-010-997-9	Sequence 9, Appl
C 43	32.4	95.3	54	1	US-08-612-551-9	Sequence 9, Appl
C 44	32.4	95.3	54	2	US-09-006-232-9	Sequence 9, Appl
C 45	32.4	95.3	54	3	US-09-211-408-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-08-484-324-3/c
; Sequence 3, Application US/08484324
; Patent No. 5654182
; GENERAL INFORMATION:
; APPLICANT: Wahl, Geoffrey M
; APPLICANT: O'Gorman, Stephen V
; TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN
; TITLE OF INVENTION: MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL
; THEREFOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,324
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9984
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-484-324-3

Query Match 95.3%; Score 32.4; DB 1; Length 34;
Best Local Similarity 97.1%; Pred. No. 6.4e-05;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAAGTTCCTATCTTCTGGAGAATAGGAATTC 34
DB 34 GAAGTTCCTATCTTCTTAGAGATAGGAATTC 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 10:55:04 ; Search time 199 Seconds
(without alignments)
1011.413 Million cell updates/sec

Title: US-10-089-380-5
Perfect score: 34
Sequence: 1 gaagttctactttcttgagaataggaacttc 34

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
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2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2002as:*
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7: Geneseq2003as:*
8: Geneseq2003bs:*
9: Geneseq2003cs:*
10: Geneseq2003ds:*
11: Geneseq2004as:*
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13: Geneseq2004cs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	34	AAF87359	Aaf87359 Yeast FRT
2	34	100.0	52	AAF87369	Aaf87369 Mutant FRT
3	34	100.0	52	AAF87378	Aaf87378 Mutant FRT
4	32.4	95.3	34	AAT92196	Aat92196 S. cerevi
5	32.4	95.3	34	AAV43562	AAV43562 FLP recom
6	32.4	95.3	34	AAV61227	AAV61227 Wild type
7	32.4	95.3	34	AAV72331	AAV72331 Wild type
8	32.4	95.3	34	AAV72331	AAV72331 Wild type
9	32.4	95.3	34	AAV72331	AAV72331 Wild type
10	32.4	95.3	34	AAV72331	AAV72331 Wild type
11	32.4	95.3	34	AAV72331	AAV72331 Wild type
12	32.4	95.3	34	AAV72331	AAV72331 Wild type
13	32.4	95.3	34	AAV72331	AAV72331 Wild type
14	32.4	95.3	34	AAV72331	AAV72331 Wild type
15	32.4	95.3	34	AAV72331	AAV72331 Wild type
16	32.4	95.3	34	AAV72331	AAV72331 Wild type
17	32.4	95.3	34	AAV72331	AAV72331 Wild type
18	32.4	95.3	34	AAV72331	AAV72331 Wild type
19	32.4	95.3	34	AAV72331	AAV72331 Wild type
20	32.4	95.3	34	AAV72331	AAV72331 Wild type

C 21	32.4	95.3	34	6	AA46212	Yeast FRT
C 22	32.4	95.3	34	6	AA46212	Yeast FRT
C 23	32.4	95.3	34	6	AA46212	Yeast FRT
C 24	32.4	95.3	34	6	AA46212	Yeast FRT
C 25	32.4	95.3	34	6	AA46212	Yeast FRT
C 26	32.4	95.3	34	6	AA46212	Yeast FRT
C 27	32.4	95.3	34	6	AA46212	Yeast FRT
C 28	32.4	95.3	34	6	AA46212	Yeast FRT
C 29	32.4	95.3	34	6	AA46212	Yeast FRT
C 30	32.4	95.3	34	6	AA46212	Yeast FRT
C 31	32.4	95.3	34	6	AA46212	Yeast FRT
C 32	32.4	95.3	34	6	AA46212	Yeast FRT
C 33	32.4	95.3	34	6	AA46212	Yeast FRT
C 34	32.4	95.3	34	6	AA46212	Yeast FRT
C 35	32.4	95.3	34	6	AA46212	Yeast FRT
C 36	32.4	95.3	34	6	AA46212	Yeast FRT
C 37	32.4	95.3	34	6	AA46212	Yeast FRT
C 38	32.4	95.3	34	6	AA46212	Yeast FRT
C 39	32.4	95.3	34	6	AA46212	Yeast FRT
C 40	32.4	95.3	34	6	AA46212	Yeast FRT
C 41	32.4	95.3	34	6	AA46212	Yeast FRT
C 42	32.4	95.3	34	6	AA46212	Yeast FRT
C 43	32.4	95.3	34	6	AA46212	Yeast FRT
C 44	32.4	95.3	34	6	AA46212	Yeast FRT
C 45	32.4	95.3	34	6	AA46212	Yeast FRT

ALIGNMENTS

RESULT 1
AAF87359
ID AAF87359 standard; DNA; 34 BP.
XX
AC AAF87359;
XX
DT 09-JUL-2001 (first entry)
XX
DE Yeast FRT sequence variant #4.
XX
KW Yeast; FRT; gene therapy; gene insertion; gene replacement;
KW DNA recombination; recombinase; FLP; transgenic animal; variant; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200123545-A1.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-JP006686.
XX
PR 30-SEP-1999; 99JP-00280210.
PR 06-DEC-1999; 99JP-00346727.
XX
XX (SUMU) SUMITOMO PHARM CO LTD.
XX (SAIT) SAITO I.
XX Saito I, Kanegae Y;
XX WPI, 2001-266149/27.
XX Variant FRT sequences useful for in vivo gene therapy comprises central 8 base spacer sequence.
XX Disclosure; Page 58; 73pp; Japanese.

The present sequence is a variant of the FRT sequence from Saccharomyces cerevisiae. Variant FRT sequences may be used in a method of performing highly efficient gene insertion or gene replacement. The variant FRT sequences each undergo a recombination reaction with another variant FRT of the same sequence in the presence of recombinase FLP. The method is useful for producing transgenic animal cells and animals. By locally inserting the DNA and recombinase FLP, genes can be targeted to specific

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 10:58:49 ; Search time. 741.75 Seconds
(without alignments)
2221.068 Million cell updates/sec

Title: US-10-089-380-5
Perfect score: 34
Sequence: 1 gaagttctatactttctggagaataggaacttc 34

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_hg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	34	6	BD013288 DNA compr
2	34	100.0	52	6	BD013298 DNA compr
3	34	100.0	52	6	BD013307 DNA compr
4	32.4	95.3	34	6	AS9775 Sequence 2
5	32.4	95.3	34	6	AR067801 Sequence
6	32.4	95.3	34	6	AR105498 Sequence
7	32.4	95.3	34	6	AR130339 Sequence
8	32.4	95.3	34	6	AR142481 Sequence
9	32.4	95.3	34	6	BD246903 Improved
10	32.4	95.3	34	6	BD267670 Delivery
11	32.4	95.3	34	6	CQ819068 Sequence
12	32.4	95.3	34	6	E43464 Method for
13	32.4	95.3	34	6	I59685 Sequence 3
14	32.4	95.3	34	6	I69353 Sequence 3
15	32.4	95.3	34	6	AR194975 Sequence
16	32.4	95.3	34	6	AR232395 Sequence
17	32.4	95.3	34	6	AR234678 Sequence
18	32.4	95.3	34	6	AR264370 Sequence
19	32.4	95.3	34	6	AR302446 Sequence

C 20	32.4	95.3	34	6	AR302544	AR302544 Sequence
C 21	32.4	95.3	34	6	AR307970	AR307970 Sequence
C 22	32.4	95.3	34	6	AR342117	AR342117 Sequence
C 23	32.4	95.3	34	6	AR370679	AR370679 Sequence
C 24	32.4	95.3	34	6	AR403690	AR403690 Sequence
C 25	32.4	95.3	34	6	AR438854	AR438854 Sequence
C 26	32.4	95.3	34	6	AR477307	AR477307 Sequence
C 27	32.4	95.3	34	6	AR494802	AR494802 Sequence
C 28	32.4	95.3	34	6	AR527595	AR527595 Sequence
C 29	32.4	95.3	34	6	AX101007	AX101007 Sequence
C 30	32.4	95.3	34	6	AX269147	AX269147 Sequence
C 31	32.4	95.3	34	6	AX359678	AX359678 Sequence
C 32	32.4	95.3	34	6	AX453121	AX453121 Sequence
C 33	32.4	95.3	34	6	AX555208	AX555208 Sequence
C 34	32.4	95.3	34	6	AX657059	AX657059 Sequence
C 35	32.4	95.3	34	6	AX657060	AX657060 Sequence
C 36	32.4	95.3	34	6	BD013284	BD013284 DNA compr
C 37	32.4	95.3	34	6	BD013285	BD013285 DNA compr
C 38	32.4	95.3	34	6	BD083074	BD083074 Antisense
C 39	32.4	95.3	34	6	BD093613	BD093613 Antisense
C 40	32.4	95.3	34	6	BD094631	BD094631 Method fo
C 41	32.4	95.3	35	6	BD271118	BD271118 Methods f
C 42	32.4	95.3	36	6	E43477	E43477 Method for
C 43	32.4	95.3	36	6	AR527608	AR527608 Sequence
C 44	32.4	95.3	36	6	BD094644	BD094644 Method fo
C 45	32.4	95.3	39	6	AX377747	AX377747 Sequence

ALIGNMENTS

RESULT 1
BD013288
LOCUS BD013288 34 bp DNA linear PAT 02-AUG-2002
DEFINITION DNA comprising mutant FRT sequence.
ACCESSION BD013288
VERSION BD013288.1 GI:22093477
KEYWORDS WO 0123545-A/5.
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

REFERENCE 1 (bases 1 to 34)
AUTHORS Saito, I. and Kanegae, Y.
TITLES DNA comprising mutant FRT sequence
JOURNAL Patent: WO 0123545-A 5 05-APR-2001;
IZUMU SAITO, SUMITOMO PHARMACEUTICALS CO LTD, YUMI KANEGAE
COMMENT OS Saccharomyces cerevisiae (yeast)
PN WO 0123545-A/5
PD 05-APR-2001
PF 28-SEP-2000 WO 2000JP06686
PR 30-SEP-1999 JP 99P 280210, 06-DEC-1999 JP 99P 346727 PI

IZUMU SAITO, YUMI KANEGAE
PC C12N15/11, C12N15/10, A01K67/027, A61K48/00
CC DNA comprising mutant FRT sequence
FH Key Location/Qualifiers
FT source 1..34
FT Location/Qualifiers
/organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
/db_xref="taxon:4932"

FEATURES
source 1..34

ORIGIN

Query Match 100.0%; Score 34; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAGTTCTATCTTCTGGAGAAATAGGAATTC 34
Db 1 GAAGTTCTATCTTCTGGAGAAATAGGAATTC 34

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 12:20:40 ; Search time 1692 seconds
(without alignments)
764.885 Million cell updates/sec

Title: US-10-089-380-4

Perfect score: 34

Sequence: 1 gaagttctatactatcttgagaataggaaacttc 34

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*

2: gb_est2.*

3: gb_hcc.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gsl1.*

9: gb_gsl2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	30.8	90.6	74	9	CG654127 OST420864
C 2	30.8	90.6	81	1	A1265023
C 3	30.8	90.6	81	1	A1265111 uk01f07.y
C 4	30.8	90.6	81	1	A1272501 uk04g01.y
C 5	30.8	90.6	88	1	A1316311 uj99a11.y
C 6	30.8	90.6	106	9	CG548652 OST150646
C 7	30.8	90.6	112	9	CG606396 OST284215
C 8	30.8	90.6	124	9	CG529627 OST110354
C 9	30.8	90.6	130	9	CG526837 OST103896
C 10	30.8	90.6	133	9	CG529602 OST110285
C 11	30.8	90.6	135	9	CG552967 OST164977
C 12	30.8	90.6	139	9	CG495088 OST134325
C 13	30.8	90.6	140	9	CG667250 OST459771
C 14	30.8	90.6	146	9	CG589974 OST242842
C 15	30.8	90.6	151	9	CG666807 OST457802
C 16	30.8	90.6	153	9	CG523992 OST97396
C 17	30.8	90.6	161	9	CG609937 OST291997
C 18	30.8	90.6	162	9	CG536645 OST124810
C 19	30.8	90.6	168	9	CG529685 OST110501
C 20	30.8	90.6	175	9	CR202574 Forward s
C 21	30.8	90.6	182	9	CG522772 OST92942
C 22	30.8	90.6	182	9	CG526410 OST102968
C 23	30.8	90.6	189	9	CG528753 OST108468
C 24	30.8	90.6	194	9	CG671483 OST500326

C 25	30.8	90.6	206	9	CG668768
C 26	30.8	90.6	208	9	CR069250
C 27	30.8	90.6	216	9	CG573772
C 28	30.8	90.6	216	9	CG579328
C 29	30.8	90.6	219	9	CG667178
C 30	30.8	90.6	222	9	CR271082
C 31	30.8	90.6	228	9	CG669744
C 32	30.8	90.6	239	9	CG667464
C 33	30.8	90.6	241	9	CG670326
C 34	30.8	90.6	253	9	CG527478
C 35	30.8	90.6	254	9	CG667921
C 36	30.8	90.6	279	9	CG670404
C 37	30.8	90.6	280	9	CG545746
C 38	30.8	90.6	281	9	CG667916
C 39	30.8	90.6	285	9	CG66517
C 40	30.8	90.6	285	9	CG666761
C 41	30.8	90.6	293	9	CG666889
C 42	30.8	90.6	306	9	CG666905
C 43	30.8	90.6	314	9	CG557567
C 44	30.8	90.6	314	9	CG668319
C 45	30.8	90.6	316	9	CG667495

ALIGNMENTS

RESULT 1
CG654127/c

LOCUS

DEFINITION

CG654127

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 74

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129Sv/Ev"

/db_xref="taxon:10090"

/clone="OST420864"

/cell_type="embryonic stem cell"

/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match

Best Local Similarity

Matches

32; Conservative

0; Mismatches

2; Indels

0; Gaps

0;

Qy

1 GAAGTTCTATCTTCTGGAATAGGAACCTC 34

CG654127 74 bp mRNA linear GSS 02-OCT-2003
OST420864 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST420864,
mRNA sequence.

CG654127

CG654127.1 GI:37477976

GSS.

Mus musculus (house mouse)

Mus musculus

1 (bases 1 to 74)

Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,

Piggott, J., Beltrando, R.H., Buxton, E.C., Edwards, J., Finch, R.A.,

Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,

Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,

Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,

Sparks, M.J., Van Slightenhorst, I., Vogel, P., Walke, W., Xu, N.,

Zhu, Q., Person, C. and Sands, A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap

screen to identify potential targets for therapeutic intervention

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

Contact: Zambrowicz BP

OmniBank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as

described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

Location/Qualifiers

1. 74

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129Sv/Ev"

/db_xref="taxon:10090"

/clone="OST420864"

/cell_type="embryonic stem cell"

/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match

Best Local Similarity

Matches

32; Conservative

0; Mismatches

2; Indels

0; Gaps

0;

Qy

1 GAAGTTCTATCTTCTGGAATAGGAACCTC 34

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 15:17:50 ; Search time 306.75 Seconds
(without alignments)
718.497 Million cell updates/sec

Title: US-10-089-380-4
Perfect score: 34
Sequence: 1 gaagttctatactatcttgagaatgaacttc 34

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
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21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
C 1	30.8	90.6	34	8	US-08-866-279A-14
C 2	30.8	90.6	34	9	US-09-920-932-2
C 3	30.8	90.6	34	9	US-09-804-653-7
C 4	30.8	90.6	34	9	US-09-748-739A-24
C 5	30.8	90.6	34	9	US-09-822-634-18
C 6	30.8	90.6	34	10	US-09-948-193-5
C 7	30.8	90.6	34	10	US-09-997-209-90

C 8	30.8	90.6	34	13	US-10-086-542A-3
C 9	30.8	90.6	34	15	US-10-005-602-5
C 10	30.8	90.6	34	15	US-10-353-445-10
C 11	30.8	90.6	34	16	US-10-368-442-7
C 12	30.8	90.6	34	17	US-10-430-907-1
C 13	30.8	90.6	34	17	US-10-430-908-1
C 14	30.8	90.6	34	17	US-10-440-030-1
C 15	30.8	90.6	34	17	US-10-378-064-4
C 16	30.8	90.6	34	17	US-10-444-664-3
C 17	30.8	90.6	34	18	US-10-639-751-1
C 18	30.8	90.6	34	18	US-10-433-206-90
C 19	30.8	90.6	34	19	US-10-649-547-19
C 20	30.8	90.6	34	20	US-10-623-386-18
C 21	30.8	90.6	34	20	US-10-846-700-14
C 22	30.8	90.6	34	21	US-10-469-508-44
C 23	30.8	90.6	34	21	US-10-976-042-39
C 24	30.8	90.6	34	22	US-10-954-721-18
C 25	30.8	90.6	42	10	US-09-843-150-24
C 26	30.8	90.6	42	10	US-09-843-150-25
C 27	30.8	90.6	42	18	US-10-270-176-55
C 28	30.8	90.6	42	20	US-10-475-962-24
C 29	30.8	90.6	42	20	US-10-475-962-25
C 30	30.8	90.6	48	8	US-08-866-279A-15
C 31	30.8	90.6	48	9	US-09-351-819-2
C 32	30.8	90.6	48	15	US-10-206-163-2
C 33	30.8	90.6	48	15	US-10-161-403-62
C 34	30.8	90.6	48	15	US-10-161-403-63
C 35	30.8	90.6	48	16	US-10-252-279-3
C 36	30.8	90.6	48	20	US-10-846-700-15
C 37	30.8	90.6	54	8	US-08-866-279A-3
C 38	30.8	90.6	54	20	US-10-846-700-3
C 39	30.8	90.6	58	10	US-09-843-150-32
C 40	30.8	90.6	58	10	US-09-843-150-33
C 41	30.8	90.6	58	16	US-10-182-616-29
C 42	30.8	90.6	58	16	US-10-182-616-30
C 43	30.8	90.6	58	20	US-10-475-962-32
C 44	30.8	90.6	58	20	US-10-475-962-33
C 45	30.8	90.6	59	8	US-08-866-279A-2

ALIGNMENTS

RESULT 1
US-08-866-279A-14/c
; Sequence 14, Application US/08866279A
; Publication No. US20020170076A1
; GENERAL INFORMATION:
; APPLICANT: Susan DYMECKI
; TITLE OF INVENTION: Use of Flp Recombinase in Mice
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/866, 279A
; FILING DATE: 30-MAY-1997
; CLASSIFICATION: 800
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 13:28:42 ; Search time 59.5 Seconds
(without alignments)
935.015 Million cell updates/sec

Title: US-10-089-380-4

Perfect score: 34

Sequence: 1 gaagttcctatactatcttgagaataggaaattc 34

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/5A COMB.seq:*
- 2: /cgn2_6/prodata/1/ina/5B COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/PCTUS COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	30.8	90.6	34	1	US-08-484-324-3
C 2	30.8	90.6	34	1	US-08-486-409-3
C 3	30.8	90.6	34	2	US-08-864-224-18
C 4	30.8	90.6	34	2	US-08-975-763-3
C 5	30.8	90.6	34	2	US-08-925-784-3
C 6	30.8	90.6	34	2	US-08-972-258-4
C 7	30.8	90.6	34	3	US-09-011-257-2
C 8	30.8	90.6	34	3	US-08-745-404-5
C 9	30.8	90.6	34	3	US-09-263-128-4
C 10	30.8	90.6	34	3	US-09-193-502-1
C 11	30.8	90.6	34	3	US-09-193-503B-10
C 12	30.8	90.6	34	3	US-09-193-475-3
C 13	30.8	90.6	34	3	US-09-193-484-1
C 14	30.8	90.6	34	3	US-09-563-239-2
C 15	30.8	90.6	34	3	US-09-438-874A-1
C 16	30.8	90.6	34	3	US-09-439-158-1
C 17	30.8	90.6	34	4	US-09-415-839-10
C 18	30.8	90.6	34	4	US-09-718-034-1
C 19	30.8	90.6	34	4	US-09-606-323C-4
C 20	30.8	90.6	34	4	US-09-438-239-1
C 21	30.8	90.6	34	4	US-09-439-042A-1
C 22	30.8	90.6	34	4	US-09-455-050A-1
C 23	30.8	90.6	34	4	US-09-411-826-3
C 24	30.8	90.6	34	4	US-09-793-372-19
C 25	30.8	90.6	34	4	US-09-641-111A-4
C 26	30.8	90.6	34	4	US-09-869-185B-1
C 27	30.8	90.6	34	4	US-09-937-837-8

C 28	30.8	90.6	34	4	US-08-866-279A-14	Sequence 14, Appl
C 29	30.8	90.6	34	4	US-09-122-384-18	Sequence 18, Appl
C 30	30.8	90.6	34	5	PCT-US92-01899-3	Sequence 3, Appl
C 31	30.8	90.6	36	4	US-09-869-185B-14	Sequence 14, Appl
C 32	30.8	90.6	40	4	US-09-869-185B-11	Sequence 11, Appl
C 33	30.8	90.6	40	4	US-09-869-185B-12	Sequence 12, Appl
C 34	30.8	90.6	44	4	US-08-869-185B-13	Sequence 13, Appl
C 35	30.8	90.6	48	4	US-08-866-279A-15	Sequence 15, Appl
C 36	30.8	90.6	51	3	US-09-837-863-3	Sequence 3, Appl
C 37	30.8	90.6	51	3	US-09-837-863-4	Sequence 4, Appl
C 38	30.8	90.6	52	3	US-09-837-863-11	Sequence 11, Appl
C 39	30.8	90.6	52	3	US-09-837-863-12	Sequence 12, Appl
C 40	30.8	90.6	53	3	US-09-837-863-5	Sequence 5, Appl
C 41	30.8	90.6	53	3	US-09-837-863-6	Sequence 6, Appl
C 42	30.8	90.6	54	1	US-08-010-997-9	Sequence 9, Appl
C 43	30.8	90.6	54	1	US-08-612-551-9	Sequence 9, Appl
C 44	30.8	90.6	54	2	US-09-006-232-9	Sequence 9, Appl
C 45	30.8	90.6	54	3	US-09-211-408-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1

US-08-484-324-3/c

; Sequence 3, Application US/08484324

; Patent No. 5654182

; GENERAL INFORMATION:

; APPLICANT: Wahl, Geoffrey M

; TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN

; TITLE OF INVENTION: MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESS: Pretty, Schroeder, Brueggemann & Clark

; STREET: 444 South Flower Street, Suite 2000

; CITY: Los Angeles

; STATE: California

; COUNTRY: USA

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/484,324

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Reiter, Stephen E

; REGISTRATION NUMBER: 31,192

; REFERENCE/DOCKET NUMBER: P41 9984

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 546-4737

; TELEFAX: (619) 546-9392

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-484-324-3

Query Match 90.6%; Score 30.8; DB 1; Length 34;

Best Local Similarity 94.1%; Pred. No. 0.00062;

Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAGTTCCTATACTATCTTGAGAATAGGAATTC 34

DB 34 GAAGTTCCTATACTATCTTGAGAATAGGAATTC 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 10:55:04 ; Search time 199 Seconds
(without alignments)
1011.413 Million cell updates/sec

Title: US-10-089-380-4

Perfect score: 34

Sequence: 1 gaagtctactatcttgagaataggaaattc 34

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2001bs.*

6: Geneseq2002as.*

7: Geneseq2002bs.*

8: Geneseq2003as.*

9: Geneseq2003bs.*

10: Geneseq2003cs.*

11: Geneseq2003ds.*

12: Geneseq2004as.*

13: Geneseq2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	34	4	Aaf87358
2	34	100.0	52	4	Aaf87384
3	34	100.0	52	4	Aaf87375
4	32.4	95.3	34	3	Aac63092
5	32.4	95.3	50	6	Aba97763
6	32.4	95.3	52	4	Aaf87368
7	32.4	95.3	52	4	Aaf87377
8	32.4	95.3	58	6	Aba97761
9	32.4	95.3	60	6	Aba97762
10	32.4	95.3	1359	9	ACC85347
11	32.4	95.3	1359	10	ADE34325
12	32.4	95.3	2077	9	ACC85385
13	32.4	95.3	2662	9	ACC85386
14	30.8	90.6	34	2	AAT92196
15	30.8	90.6	34	2	AAV43562
16	30.8	90.6	34	2	AXA61227
17	30.8	90.6	34	2	AAV72331
18	30.8	90.6	34	2	AAV01426
19	30.8	90.6	34	2	AAI72854
20	30.8	90.6	34	3	Aaz58072

C 21	30.8	90.6	34	3	AAC61513	Aac61513 Nucleotid
C 22	30.8	90.6	34	3	AAA10237	Aaa10237 FLP recom
C 23	30.8	90.6	34	3	AAC63090	Aac63090 Wild-type
C 24	30.8	90.6	34	4	AAF24488	Aaf24488 FLP recom
C 25	30.8	90.6	34	4	AAD10220	Aad10220 Minimal w
C 26	30.8	90.6	34	4	AAF81218	Aaf81218 FLP recom
27	30.8	90.6	34	4	AAF87356	Aaf87356 Yeast FRT
28	30.8	90.6	34	4	AAF87359	Aaf87359 Yeast FRT
29	30.8	90.6	34	4	AAF87362	Aaf87362 Yeast FRT
30	30.8	90.6	34	4	AAF87355	Aaf87355 Yeast FRT
31	30.8	90.6	34	4	AAH21799	Aah21799 Saccharom
32	30.8	90.6	34	5	AAS14781	Aas14781 FLP recom
C 33	30.8	90.6	34	6	AAD46212	Aad46212 Yeast FRT
C 34	30.8	90.6	34	6	AAD24140	Aad24140 Recombina
C 35	30.8	90.6	34	6	AAD35275	Aad35275 FRT recog
C 36	30.8	90.6	34	6	ABA03777	Aba03777 Saccharom
C 37	30.8	90.6	34	6	AAD41158	Aad41158 Yeast tar
C 38	30.8	90.6	34	6	AAL49298	Aal49298 FLP recom
C 39	30.8	90.6	34	7	ADL18609	Adl18609 FRT site
C 40	30.8	90.6	34	8	ABX13963	Abx13963 Yeast FLP
41	30.8	90.6	34	8	ADA88940	Ada88940 FLP recog
C 42	30.8	90.6	34	8	ABX93111	Abx93111 Minimal F
C 43	30.8	90.6	34	9	ACC85315	Acc85315 Recombina
C 44	30.8	90.6	34	9	ACD26382	Acd26382 FRT recom
C 45	30.8	90.6	34	10	ADC17306	Adc17306 Baker's y

ALIGNMENTS

RESULT 1

AAF87358
ID AAF87358 standard; DNA; 34 BP.

XX AAF87358;

XX 09-JUL-2001 (first entry)

XX Yeast FRT sequence variant #3.

XX Yeast; FRT; gene therapy; gene insertion; gene replacement;

KW DNA recombination; recombinase; FLP; transgenic animal; variant; ds.

XX Saccharomyces cerevisiae.

XX WO200123545-A1.

XX 05-APR-2001.

XX 28-SEP-2000; 2000WO-JP006686.

XX 30-SEP-1999; 99JP-00280210.

XX 06-DEC-1999; 99JP-00346727.

XX (SUMU) SUMITOMO PHARM CO LTD.

XX (SAIT/) SAITO I.

PI Saito I, Kanegae Y;

XX WPI; 2001-266149/27.

XX Variant FRT sequences useful for in vivo gene therapy comprises central 8

XX base spacer sequence.

XX Disclosure; Page 57; 73pp; Japanese.

XX The present sequence is a variant of the FRT sequence from Saccharomyces cerevisiae. Variant FRT sequences may be used in a method of performing highly efficient gene insertion or gene replacement. The variant FRT sequences each undergo a recombination reaction with another variant FRT of the same sequence in the presence of recombinase FLP. The method is useful for producing transgenic animal cells and animals. By locally inserting the DNA and recombinase FLP, genes can be targeted to specific

Result No.	Score	Query Match	Length	DB	ID	Description	
1	34	100.0	34	6	BD013287	DNA compr	
2	34	100.0	52	6	BD013304	DNA compr	
3	34	100.0	52	6	BD013313	DNA compr	
C	34	100.0	52	6	BD013329	DNA compr	
4	32.4	95.3	32	6	BD013306	DNA compr	
C	32.4	95.3	52	6	BD013306	DNA compr	
5	32.4	95.3	1359	6	AX798126	Sequence	
C	32.4	95.3	1359	6	AX798910	Sequence	
6	32.4	95.3	2077	6	AX798172	Sequence	
C	32.4	95.3	2662	6	AX798173	Sequence	
7	32.4	95.3	34	6	A59775	Sequence 2	
C	30.8	90.6	34	6	AR067801	Sequence	
8	30.8	90.6	34	6	AR105498	Sequence	
C	30.8	90.6	34	6	AR130339	Sequence	
9	30.8	90.6	34	6	AR142481	Sequence	
C	30.8	90.6	34	6	BD246903	Improved	
10	30.8	90.6	34	6	BD267670	Delivery	
C	30.8	90.6	34	6	CQ819068	Sequence	
11	30.8	90.6	34	6	E43464	Method for	
C	30.8	90.6	34	6	I59685	Sequence 3	

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 12:20:40 ; Search time 1692 Seconds
(without alignments)
764.885 Million cell updates/sec

Title: US-10-089-380-3

Perfect score: 34

Sequence: 1 gaagttcctatactctccagagaataggaaacttc 34

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_est1.*

2: gb_est2.*

3: gb_est3.*

4: gb_est4.*

5: gb_est5.*

6: gb_est6.*

7: gb_est7.*

8: gb_gsl1.*

9: gb_gsl2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	30.8	90.6	74	9	CG654127 OST420864
C 2	30.8	90.6	81	1	AI265023 uk01f07.y
C 3	30.8	90.6	81	1	AI265111 uk03c08.y
C 4	30.8	90.6	81	1	AI272501 uk04g01.y
C 5	30.8	90.6	88	1	AI316311 u99a11.y
C 6	30.8	90.6	106	9	CG548652 OST150646
C 7	30.8	90.6	112	9	CG506396 OST284215
C 8	30.8	90.6	124	9	CG529627 OST110354
C 9	30.8	90.6	130	9	CG526837 OST103896
C 10	30.8	90.6	133	9	CG529602 OST110285
C 11	30.8	90.6	135	9	CG552967 OST164977
C 12	30.8	90.6	139	9	CG495088 OST34325
C 13	30.8	90.6	140	9	CG667250 OST459771
C 14	30.8	90.6	146	9	CG589974 OST242842
C 15	30.8	90.6	151	9	CG666807 OST457802
C 16	30.8	90.6	153	9	CG523992 OST97396
C 17	30.8	90.6	161	9	CG609937 OST291997
C 18	30.8	90.6	162	9	CG536645 OST124810
C 19	30.8	90.6	168	9	CG529685 OST110501
C 20	30.8	90.6	175	9	CR202574 Forward s
C 21	30.8	90.6	182	9	CG522772 OST92942
C 22	30.8	90.6	182	9	CG526410 OST102968
C 23	30.8	90.6	189	9	CG528753 OST108468
C 24	30.8	90.6	194	9	CG671483 OST500326

C 25	30.8	90.6	206	9	CG668768
C 26	30.8	90.6	208	9	CG69250
C 27	30.8	90.6	216	9	CG573772
C 28	30.8	90.6	216	9	CG579328
C 29	30.8	90.6	219	9	CG667178
C 30	30.8	90.6	222	9	CR271082
C 31	30.8	90.6	228	9	CG669744
C 32	30.8	90.6	239	9	CG667464
C 33	30.8	90.6	241	9	CG670326
C 34	30.8	90.6	253	9	CG527478
C 35	30.8	90.6	254	9	CG667921
C 36	30.8	90.6	279	9	CG670404
C 37	30.8	90.6	280	9	CG545746
C 38	30.8	90.6	281	9	CG667916
C 39	30.8	90.6	285	9	CG666517
C 40	30.8	90.6	285	9	CG666761
C 41	30.8	90.6	293	9	CG666889
C 42	30.8	90.6	306	9	CG666905
C 43	30.8	90.6	314	9	CG557567
C 44	30.8	90.6	314	9	CG668319
C 45	30.8	90.6	316	9	CG667495

ALIGNMENTS

RESULT 1
LOCUS CG654127/c
DEFINITION OST420864 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST420864, mRNA sequence.
ACCESSION CG654127
VERSION CG654127.1 GI:37477976
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 74)
AUTHORS Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J., Figgott,J., BeltrandelRio,H., Buxton,E.C., Edwards,V., Finch,R.A., Fiddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jiang,C., Key,B.W. Jr., Kipp,P.G., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Slightenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.
TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES

source
1..74
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/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST420864"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 90.6%; Score 30.8; DB 9; Length 74;
Best Local Similarity 94.1%; Pred. No. 0.033;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAGTTCTTACTCTCCAGAGAAAGAACTTC 34

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 15:17:50 ; Search time 306.75 Seconds
(without alignments)
718.497 Million cell updates/sec

Title: US-10-089-380-3

Perfect score: 34

Sequence: 1 gaagtctactctcagagaataggaattc 34

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	30.8	90.6	34	8	US-08-866-279A-14
C 2	30.8	90.6	34	9	US-09-920-932-2
C 3	30.8	90.6	34	9	US-09-804-653-7
C 4	30.8	90.6	34	9	US-09-748-739A-24
C 5	30.8	90.6	34	9	US-09-822-634-18
C 6	30.8	90.6	34	10	US-09-948-193-5
C 7	30.8	90.6	34	10	US-09-997-209-90
C 1	30.8	90.6	34	8	Sequence 14, Appl
C 2	30.8	90.6	34	9	Sequence 2, Appl
C 3	30.8	90.6	34	9	Sequence 7, Appl
C 4	30.8	90.6	34	9	Sequence 24, Appl
C 5	30.8	90.6	34	9	Sequence 18, Appl
C 6	30.8	90.6	34	10	Sequence 5, Appl
C 7	30.8	90.6	34	10	Sequence 90, Appl

C 8	30.8	90.6	34	13	US-10-086-542A-3
C 9	30.8	90.6	34	15	US-10-005-602-5
C 10	30.8	90.6	34	15	US-10-353-445-10
C 11	30.8	90.6	34	16	US-10-368-442-7
C 12	30.8	90.6	34	17	US-10-430-907-1
C 13	30.8	90.6	34	17	US-10-430-908-1
C 14	30.8	90.6	34	17	US-10-440-030-1
C 15	30.8	90.6	34	17	US-10-378-064-4
C 16	30.8	90.6	34	17	US-10-444-664-3
C 17	30.8	90.6	34	18	US-10-639-751-1
C 18	30.8	90.6	34	18	US-10-433-206-90
C 19	30.8	90.6	34	19	US-10-549-547-19
C 20	30.8	90.6	34	20	US-10-623-386-18
C 21	30.8	90.6	34	20	US-10-846-700-14
C 22	30.8	90.6	34	21	US-10-469-508-44
C 23	30.8	90.6	34	21	US-10-976-042-39
C 24	30.8	90.6	34	22	US-10-954-721-18
C 25	30.8	90.6	42	10	US-09-843-150-24
C 26	30.8	90.6	42	10	US-09-843-150-25
C 27	30.8	90.6	42	18	US-10-270-176-55
C 28	30.8	90.6	42	20	US-10-475-962-24
C 29	30.8	90.6	42	20	US-10-475-962-25
C 30	30.8	90.6	48	8	US-08-866-279A-15
C 31	30.8	90.6	48	9	US-09-351-819-2
C 32	30.8	90.6	48	15	US-10-206-163-2
C 33	30.8	90.6	48	15	US-10-161-403-62
C 34	30.8	90.6	48	15	US-10-161-403-63
C 35	30.8	90.6	48	16	US-10-252-279-3
C 36	30.8	90.6	48	20	US-10-846-700-15
C 37	30.8	90.6	54	8	US-08-866-279A-3
C 38	30.8	90.6	54	20	US-10-846-700-3
C 39	30.8	90.6	58	10	US-09-843-150-32
C 40	30.8	90.6	58	10	US-09-843-150-33
C 41	30.8	90.6	58	16	US-10-182-616-29
C 42	30.8	90.6	58	16	US-10-182-616-30
C 43	30.8	90.6	58	20	US-10-475-962-32
C 44	30.8	90.6	58	20	US-10-475-962-33
C 45	30.8	90.6	59	8	US-08-866-279A-2

ALIGNMENTS

RESULT 1
US-08-866-279A-14/c
; Sequence 14, Application US/08866279A
; Publication No. US0020170076A1
; GENERAL INFORMATION:
; APPLICANT: Susan DYMECKI
; TITLE OF INVENTION: Use of Flp Recombinase in Mice
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/866,279A
; FILING DATE: 30-MAY-1997
; CLASSIFICATION: 800
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 13:28:42 ; Search time 59.5 Seconds
(without alignments)
935.015 Million cell updates/sec

Title: US-10-089-380-3

Perfect score: 34

Sequence: 1 gaagttctactctccagagaataggaacttc 34

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA.*

1: /cgm2_6/ptodata/1/ina/5A COMB.seq.*

2: /cgm2_6/ptodata/1/ina/5B COMB.seq.*

3: /cgm2_6/ptodata/1/ina/6A COMB.seq.*

4: /cgm2_6/ptodata/1/ina/6B COMB.seq.*

5: /cgm2_6/ptodata/1/ina/PTUS COMB.seq.*

6: /cgm2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	30.8	90.6	34	1	US-08-484-324-3
C 2	30.8	90.6	34	1	US-08-486-409-3
C 3	30.8	90.6	34	2	US-08-864-224-18
C 4	30.8	90.6	34	2	US-08-975-763-3
C 5	30.8	90.6	34	2	US-08-825-784-3
C 6	30.8	90.6	34	2	US-08-972-258-4
C 7	30.8	90.6	34	3	US-09-011-257-2
C 8	30.8	90.6	34	3	US-08-745-404-5
C 9	30.8	90.6	34	3	US-09-263-128-4
C 10	30.8	90.6	34	3	US-09-193-502-1
C 11	30.8	90.6	34	3	US-09-193-503B-10
C 12	30.8	90.6	34	3	US-09-193-475-3
C 13	30.8	90.6	34	3	US-09-193-484-1
C 14	30.8	90.6	34	3	US-09-563-239-2
C 15	30.8	90.6	34	3	US-09-438-874A-1
C 16	30.8	90.6	34	3	US-09-439-158-1
C 17	30.8	90.6	34	4	US-09-415-839-10
C 18	30.8	90.6	34	4	US-09-718-034-1
C 19	30.8	90.6	34	4	US-09-606-323C-4
C 20	30.8	90.6	34	4	US-09-438-239-1
C 21	30.8	90.6	34	4	US-09-439-042A-1
C 22	30.8	90.6	34	4	US-09-455-050A-1
C 23	30.8	90.6	34	4	US-09-411-826-3
C 24	30.8	90.6	34	4	US-09-793-372-19
C 25	30.8	90.6	34	4	US-09-641-111A-4
C 26	30.8	90.6	34	4	US-09-869-185B-1
C 27	30.8	90.6	34	4	US-09-937-837-8

C 28	30.8	90.6	34	4	US-08-866-279A-14	Sequence 14, Appl
C 29	30.8	90.6	34	4	US-09-122-384-18	Sequence 18, Appl
C 30	30.8	90.6	34	5	PCT-US92-01899-3	Sequence 3, Appl
C 31	30.8	90.6	36	4	US-09-869-185B-14	Sequence 14, Appl
C 32	30.8	90.6	40	4	US-09-869-185B-11	Sequence 11, Appl
C 33	30.8	90.6	40	4	US-09-869-185B-12	Sequence 12, Appl
C 34	30.8	90.6	44	4	US-08-866-279A-15	Sequence 15, Appl
C 35	30.8	90.6	48	4	US-09-869-185B-13	Sequence 13, Appl
C 36	30.8	90.6	51	3	US-09-837-863-3	Sequence 3, Appl
C 37	30.8	90.6	51	3	US-09-837-863-4	Sequence 4, Appl
C 38	30.8	90.6	52	3	US-09-837-863-11	Sequence 11, Appl
C 39	30.8	90.6	52	3	US-09-837-863-12	Sequence 12, Appl
C 40	30.8	90.6	53	3	US-09-837-863-5	Sequence 5, Appl
C 41	30.8	90.6	53	3	US-09-837-863-6	Sequence 6, Appl
C 42	30.8	90.6	54	1	US-08-010-997-9	Sequence 9, Appl
C 43	30.8	90.6	54	1	US-08-612-551-9	Sequence 9, Appl
C 44	30.8	90.6	54	2	US-09-006-232-9	Sequence 9, Appl
C 45	30.8	90.6	54	3	US-09-211-408-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1

US-08-484-324-3/c

; Sequence 3, Application US/08484324

; Patent No. 5654182

; GENERAL INFORMATION:

; APPLICANT: Wahl, Geoffrey M

; APPLICANT: O'Gorman, Stephen V

; TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN

; TITLE OF INVENTION: MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL

; TITLE OF INVENTION: THEREFOR

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark

; STREET: 444 South Flower Street, Suite 2000

; CITY: Los Angeles

; STATE: California

; COUNTRY: USA

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/484,324

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Reiter, Stephen E

; REGISTRATION NUMBER: 31,192

; REFERENCE/DOCKET NUMBER: P41 9984

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 546-4737

; TELEFAX: (619) 546-9392

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-484-324-3

Query Match 90.6%; Score 30.8; DB 1; Length 34;
Best Local Similarity 94.1%; Pred. No. 9.4e-05;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAAGTTCCTACTCTCCAGAGAATAGGAACCTC 34
DB 34 GAAGTTCCTACTTCTAGAGATAGGAACCTC 1

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 10:55:04 ; Search time 199 Seconds
(without alignments)

1011.413 Million cell updates/sec

Title: US-10-089-380-3

Perfect score: 34

Sequence: 1 gaagtcctatactctccagagaataggaaattc 34

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_16Dec04.*
1: Geneseqn1990s.*
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3: Geneseqn2000s.*
4: Geneseqn2001s.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	34	4	Aaf87357 Yeast FRT
2	34	100.0	52	4	Aaf87374 Mutant FR
3	34	100.0	52	4	Aaf87383 Mutant FR
4	30.8	90.6	34	2	Aat92196 S. cerevi
5	30.8	90.6	34	2	Aav43562 FLP recom
6	30.8	90.6	34	2	Aax61227 Wild type
7	30.8	90.6	34	2	Aav72331 Wild type
8	30.8	90.6	34	2	Aax01426 2mu FRT e
9	30.8	90.6	34	2	Aai72854 Minimal F
10	30.8	90.6	34	3	Aaz58072 FLP recom
11	30.8	90.6	34	3	Aac61513 Nucleotid
12	30.8	90.6	34	3	Aaa10237 FLP recom
13	30.8	90.6	34	3	Aac63092 Mutant FR
14	30.8	90.6	34	3	Aac63090 Wild-type
15	30.8	90.6	34	4	Aaf24488 FLP recom
16	30.8	90.6	34	4	Aad10220 Minimal w
17	30.8	90.6	34	4	Aaf81218 FLP recom
18	30.8	90.6	34	4	Aaf87356 Yeast FRT
19	30.8	90.6	34	4	Aaf87355 Yeast FRT
20	30.8	90.6	34	4	Aah21799 Saccharom

21	30.8	90.6	34	5	AAS14781
22	30.8	90.6	34	6	AAD46212
23	30.8	90.6	34	6	AAD24140
24	30.8	90.6	34	6	AAD35275
25	30.8	90.6	34	6	ABA03777
26	30.8	90.6	34	6	AAD41158
27	30.8	90.6	34	6	AAL49298
28	30.8	90.6	34	7	ADL18609
29	30.8	90.6	34	8	ABX13963
30	30.8	90.6	34	8	ADA88940
31	30.8	90.6	34	8	ABX33111
32	30.8	90.6	34	9	ACC85315
33	30.8	90.6	34	9	ACD26382
34	30.8	90.6	34	10	ADC17306
35	30.8	90.6	34	10	ADD13799
36	30.8	90.6	34	10	ADD06116
37	30.8	90.6	34	10	ADD61473
38	30.8	90.6	34	10	AD881223
39	30.8	90.6	34	10	ADF65708
40	30.8	90.6	34	10	AD65098
41	30.8	90.6	34	10	ADH08623
42	30.8	90.6	34	12	ADG73217
43	30.8	90.6	34	12	ADH73015
44	30.8	90.6	34	12	ADI26304
45	30.8	90.6	34	12	ADO36182

ALIGNMENTS

RESULT 1
Aaf87357
ID Aaf87357 standard; DNA; 34 BP.
XX
AC Aaf87357;
XX
09-JUL-2001 (first entry)
XX
DE Yeast FRT sequence variant #2.
XX
KW Yeast; FRT; gene therapy; gene insertion; gene replacement;
KW DNA recombination; recombinase; FLP; transgenic animal; variant; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200123545-A1.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-JP006686.
XX
PR 30-SEP-1999; 99JP-00280210.
PR 06-DEC-1999; 99JP-00346727.
XX
(SUMU) SUMITOMO PHARM CO LTD.
(SAIT/) SAITO I.
PI Saito I, Kanegae Y;
XX
WPI; 2001-266149/27.
XX
Variant FRT sequences useful for in vivo gene therapy comprises central 8 base spacer sequence.

Disclosure; Page 57; 73pp; Japanese.

The present sequence is a variant of the FRT sequence from Saccharomyces cerevisiae. Variant FRT sequences may be used in a method of performing highly efficient gene insertion or gene replacement. The variant FRT sequences each undergo a recombination reaction with another variant FRT of the same sequence in the presence of recombinase FLP. The method is useful for producing transgenic animal cells and animals. By locally inserting the DNA and recombinase FLP, genes can be targeted to specific

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 10:58:49 ; Search time 741.75 Seconds
(without alignments)
2221.068 Million cell updates/sec

Title: US-10-089-380-3
Perfect score: 34
Sequence: 1 gaagttcttactctccagagaataggaaattc 34

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapept 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
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2: gb_htg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pi.*
9: gb_pr.*
10: gb_ro.*
11: gb_scs.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	34	6	BD013286
2	34	100.0	52	6	BD013303
3	34	100.0	52	6	BD013312
4	30.8	90.6	34	6	AS9775
5	30.8	90.6	34	6	AR067801
6	30.8	90.6	34	6	AR105498
7	30.8	90.6	34	6	AR130339
8	30.8	90.6	34	6	AR142481
9	30.8	90.6	34	6	BD246903
10	30.8	90.6	34	6	BD267670
11	30.8	90.6	34	6	CQ819068
12	30.8	90.6	34	6	E43464
13	30.8	90.6	34	6	I59685
14	30.8	90.6	34	6	I69353
15	30.8	90.6	34	6	AR194975
16	30.8	90.6	34	6	AR232395
17	30.8	90.6	34	6	AR234678
18	30.8	90.6	34	6	AR264370
19	30.8	90.6	34	6	AR302446

C 20	30.8	90.6	34	6	AR302544	Sequence
C 21	30.8	90.6	34	6	AR307970	Sequence
C 22	30.8	90.6	34	6	AR342117	Sequence
C 23	30.8	90.6	34	6	AR370679	Sequence
C 24	30.8	90.6	34	6	AR403690	Sequence
C 25	30.8	90.6	34	6	AR438854	Sequence
C 26	30.8	90.6	34	6	AR477307	Sequence
C 27	30.8	90.6	34	6	AR494802	Sequence
C 28	30.8	90.6	34	6	AR527595	Sequence
C 29	30.8	90.6	34	6	AX101007	Sequence
C 30	30.8	90.6	34	6	AX269147	Sequence
C 31	30.8	90.6	34	6	AX359678	Sequence
C 32	30.8	90.6	34	6	AX453121	Sequence
C 33	30.8	90.6	34	6	AX555208	Sequence
C 34	30.8	90.6	34	6	AX657059	Sequence
C 35	30.8	90.6	34	6	AX657060	Sequence
C 36	30.8	90.6	34	6	BD013284	DNA compr
C 37	30.8	90.6	34	6	BD013285	DNA compr
C 38	30.8	90.6	34	6	BD083074	Antisense
C 39	30.8	90.6	34	6	BD093613	Antisense
C 40	30.8	90.6	34	6	BD094631	Method fo
C 41	30.8	90.6	35	6	BD271118	Methods f
C 42	30.8	90.6	36	6	E43477	Method for
C 43	30.8	90.6	36	6	AR527608	Sequence
C 44	30.8	90.6	36	6	BD094644	Method fo
C 45	30.8	90.6	39	6	AX377747	Sequence

ALIGNMENTS

RESULT 1
LOCUS BD013286 34 bp DNA linear PAT 02-AUG-2002
DEFINITION DNA comprising mutant FRT sequence.
ACCESSION BD013286
VERSION WO 0123545-A/3
KEYWORDS Saccharomyces cerevisiae (baker's yeast)
SOURCE Saccharomyces cerevisiae
ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

REFERENCE 1 (bases 1 to 34)
AUTHORS Saito, I. and Kanegae, Y.
TITLE DNA comprising mutant FRT sequence
JOURNAL Patent: WO 0123545-A 3 05-APR-2001;
IZUMU SAITO, SUMITOMO PHARMACEUTICALS CO LTD, YUIMI KANEGAE

COMMENT OS Saccharomyces cerevisiae (yeast)
PN WO 0123545-A/3
PD 05-APR-2001
PF 28-SEP-2000 WO 2000JP006686
PR 30-SEP-1999 JP 99P 280210, 06-DEC-1999 JP 99P 346727 PI
IZUMU SAITO, YUIMI KANEGAE
PC C12N15/11, C12N15/10, A01K67/027, A61K48/00
CC DNA comprising mutant FRT sequence
FH Key Location/Qualifiers
FT source 1..34
FT /organism='Saccharomyces cerevisiae (yeast)'

FEATURES
source 1..34
/organism='Saccharomyces cerevisiae'
/mol_type='genomic DNA'
/db_xref='taxon:4932'

ORIGIN

Query Match 100.0%; Score 34; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAGTTCTTACTCTCCAGAGAATAGGAATCTC 34
|||||
Db 1 GAAGTTCTTACTCTCTCCAGAGAATAGGAATCTC 34

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 12:20:40 ; Search time 1692 Seconds
(without alignments)
764.885 Million cell updates/sec

Title: US-10-089-380-2

Perfect score: 34

Sequence: 1 gaagttcttactctctggaataaggaattc 34

Scoring table:

IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 segs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_est1:*

2: gb_est2:*

3: gb_hc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	30.8	90.6	74	9	CG654127 OST420864
C 2	30.8	90.6	81	1	A1265023 uk01f07.y
C 3	30.8	90.6	81	1	A1265111 uk03c08.y
C 4	30.8	90.6	81	1	A1272501 uk04g01.y
C 5	30.8	90.6	88	1	A1316311 uj99a11.y
C 6	30.8	90.6	106	9	CG548652 OST150646
C 7	30.8	90.6	112	9	CG606396 OST284215
C 8	30.8	90.6	124	9	CG529627 OST110354
C 9	30.8	90.6	130	9	CG526837 OST103896
C 10	30.8	90.6	133	9	CG529602 OST110285
C 11	30.8	90.6	135	9	CG552967 OST164977
C 12	30.8	90.6	139	9	CG495088 OST34325
C 13	30.8	90.6	140	9	CG667250 OST459771
C 14	30.8	90.6	146	9	CG589974 OST242842
C 15	30.8	90.6	151	9	CG666807 OST457802
C 16	30.8	90.6	153	9	CG523992 OST97396
C 17	30.8	90.6	161	9	CG609937 OST291997
C 18	30.8	90.6	162	9	CG536645 OST124810
C 19	30.8	90.6	168	9	CG529685 OST110501
C 20	30.8	90.6	175	9	CR202574 Forward s
C 21	30.8	90.6	182	9	CG522772 OST92942
C 22	30.8	90.6	182	9	CG526410 OST102968
C 23	30.8	90.6	189	9	CG528753 OST108468
C 24	30.8	90.6	194	9	CG671483 OST500326

C 25	30.8	90.6	206	9	CG668768
C 26	30.8	90.6	208	9	CR069250
C 27	30.8	90.6	216	9	CG573772
C 28	30.8	90.6	216	9	CG579328
C 29	30.8	90.6	219	9	CG667178
C 30	30.8	90.6	222	9	CR271082
C 31	30.8	90.6	228	9	CG669744
C 32	30.8	90.6	239	9	CG667464
C 33	30.8	90.6	241	9	CG670326
C 34	30.8	90.6	253	9	CG527478
C 35	30.8	90.6	254	9	CG667921
C 36	30.8	90.6	279	9	CG670404
C 37	30.8	90.6	280	9	CG545746
C 38	30.8	90.6	281	9	CG667916
C 39	30.8	90.6	285	9	CG666517
C 40	30.8	90.6	285	9	CG666761
C 41	30.8	90.6	293	9	CG666889
C 42	30.8	90.6	306	9	CG666905
C 43	30.8	90.6	314	9	CG557567
C 44	30.8	90.6	314	9	CG668319
C 45	30.8	90.6	316	9	CG667495

ALIGNMENTS

RESULT 1
CG654127/c
LOCUS OST420864 Mus musculus 129Sv/Ev Mus musculus CDNA clone OST420864,
DEFINITION mRNA sequence.
ACCESSION CG654127
VERSION CG654127.1 GI:37477976
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 74)
AUTHORS Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., Beltrandelio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Slightenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.
Wk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmniBank

Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers
1. 74
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST420864"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

TITLE
JOURNAL
COMMENT

FEATURES
source

ORIGIN

Query Match 90.6%; Score 30.8; DB 9; Length 74;
Best Local Similarity 94.1%; Pred. No. 0.035;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GAAGTTCCTACTCTCTGGAGAAAGAACTTC 34

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 13:28:42 ; Search time 59.5 Seconds
(without alignments)
935.015 Million cell updates/sec

Title: US-10-089-380-2

Perfect score: 34

Sequence: 1 gaggtctactctctggaataaggaacttc 34

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	30.8	90.6	34	1	US-08-484-324-3
C 2	30.8	90.6	34	1	US-08-486-409-3
C 3	30.8	90.6	34	2	US-08-864-224-18
C 4	30.8	90.6	34	2	US-08-975-763-3
C 5	30.8	90.6	34	2	US-08-825-784-3
C 6	30.8	90.6	34	2	US-08-972-258-4
C 7	30.8	90.6	34	3	US-09-011-257-2
C 8	30.8	90.6	34	3	US-08-745-404-5
C 9	30.8	90.6	34	3	US-09-263-128-4
C 10	30.8	90.6	34	3	US-09-193-502-1
C 11	30.8	90.6	34	3	US-09-193-503B-10
C 12	30.8	90.6	34	3	US-09-193-475-3
C 13	30.8	90.6	34	3	US-09-193-484-1
C 14	30.8	90.6	34	3	US-09-563-239-2
C 15	30.8	90.6	34	3	US-09-438-874A-1
C 16	30.8	90.6	34	3	US-09-439-158-1
C 17	30.8	90.6	34	4	US-09-415-839-10
C 18	30.8	90.6	34	4	US-09-718-034-1
C 19	30.8	90.6	34	4	US-09-606-323C-4
C 20	30.8	90.6	34	4	US-09-438-239-1
C 21	30.8	90.6	34	4	US-09-439-042A-1
C 22	30.8	90.6	34	4	US-09-455-050A-1
C 23	30.8	90.6	34	4	US-09-411-826-3
C 24	30.8	90.6	34	4	US-09-793-372-19
C 25	30.8	90.6	34	4	US-09-641-111A-4
C 26	30.8	90.6	34	4	US-09-869-185B-1
C 27	30.8	90.6	34	4	US-09-937-837-8

Sequence 14, Appl
Sequence 18, Appl
Sequence 3, Appl
Sequence 14, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 15, Appl
Sequence 3, Appl
Sequence 4, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 5, Appl
Sequence 6, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-08-484-324-3/c
Sequence 3, Application US/08484324
Patent No. 5654182
GENERAL INFORMATION:
APPLICANT: Wahl, Geoffrey M.
TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL THEREFOR
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patcin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,324
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9984
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
TELEFAX: (619) 546-9392
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-484-324-3

Query Match 90.6%; Score 30.8; DB 1; Length 34;

Best Local Similarity 94.1%; Pred. No. 0.00024;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAGTTCCTACTCTCTGGAGAAAGGAAGTTC 34

Db 34 GAAGTTCCTACTCTCTGGAGAAAGGAAGTTC 1

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 10:55:04 ; Search time 199 Seconds
(without alignments)
1011.413 Million cell updates/sec

Title: US-10-089-380-2

Perfect score: 34

Sequence: 1 gaagttctatactctctggagaataggaacttc 34

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_16Dec04:*

- 1: Geneseqn1990s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001s:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	34	4	Aaf87356 Yeast FRT
2	34	100.0	52	4	Aaf87372 Mutant FR
3	34	100.0	52	4	Aaf87381 Mutant FR
4	32.4	95.3	34	4	Aaf87359 Yeast FRT
5	32.4	95.3	52	4	Aaf87369 Mutant FR
6	32.4	95.3	52	4	Aaf87378 Mutant FR
7	30.8	90.6	34	2	Aat92196 S. cerevi
8	30.8	90.6	34	2	Aav43562 FLP recom
9	30.8	90.6	34	2	Aax61227 Wild type
10	30.8	90.6	34	2	Aav72331 Wild type
11	30.8	90.6	34	2	Aax01426 2mu FRT e
12	30.8	90.6	34	3	Aai72854 Minimal F
13	30.8	90.6	34	3	Aaz58072 FLP recom
14	30.8	90.6	34	3	Aac61513 Nucleotid
15	30.8	90.6	34	3	Aaa10237 FLP recom
16	30.8	90.6	34	3	Aac63092 Mutant FR
17	30.8	90.6	34	3	Aac63090 Wild-type
18	30.8	90.6	34	3	Aaf24488 FLP recom
19	30.8	90.6	34	4	Aad10220 Minimal w
20	30.8	90.6	34	4	Aaf81218 FLP recom

21	30.8	90.6	34	4	Aaf87358 Yeast FRT
22	30.8	90.6	34	4	Aaf87357 Yeast FRT
23	30.8	90.6	34	4	Aaf87355 Yeast FRT
24	30.8	90.6	34	4	Aah21799 Saccharom
25	30.8	90.6	34	5	Aae14781 FLP recom
26	30.8	90.6	34	6	Aad46212 Yeast FRT
27	30.8	90.6	34	6	Aad24140 Recombina
28	30.8	90.6	34	6	Aad35275 FRT recog
29	30.8	90.6	34	6	Aba03777 Saccharom
30	30.8	90.6	34	6	Aad41158 Yeast tar
31	30.8	90.6	34	6	Aal49298 FLP recom
32	30.8	90.6	34	7	Adl18609 FRT site
33	30.8	90.6	34	8	Adx13963 Yeast FLP
34	30.8	90.6	34	8	Ada88940 FLP recog
35	30.8	90.6	34	8	Adx93111 Minimal F
36	30.8	90.6	34	9	Acc85315 Recombina
37	30.8	90.6	34	9	Adc26382 FRT recom
38	30.8	90.6	34	10	Adc17306 Baker's Y
39	30.8	90.6	34	10	Adcl1799 Oligonucl
40	30.8	90.6	34	10	Ado06116 Yeast fli
41	30.8	90.6	34	10	Ad61473 FLP recom
42	30.8	90.6	34	10	Ad61223 FLP recom
43	30.8	90.6	34	10	Adf65708 FLP-recog
44	30.8	90.6	34	10	Ad65098 FRT recom
45	30.8	90.6	34	10	Adh08623 Yeast FLP

ALIGNMENTS

RESULT 1

Aaf87356
ID Aaf87356 standard; DNA; 34 BP.
XX
AC Aaf87356;
XX
DT 09-JUL-2001 (first entry)
XX
DS Yeast FRT sequence variant #1.
XX
KW Yeast; FRT; gene therapy; gene insertion; gene replacement;
KW DNA recombination; recombinase; FLP; transgenic animal; variant; ds.
OS Saccharomyces cerevisiae.
XX
FN WO200123545-A1.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-JP006686.
XX
PR 30-SEP-1999; 99JP-00280210.
PR 06-DEC-1999; 99JP-00346727.

(SUMU) SUMITOMO PHARM CO LTD.
(SAIT/) SAITO I.

Saito I, Kanegae Y;

WPI; 2001-266149/27.

Variant FRT sequences useful for in vivo gene therapy comprises central 8 base spacer sequence.

Disclosure; Page 57; 73pp; Japanese.

The present sequence is a variant of the FRT sequence from Saccharomyces cerevisiae. Variant FRT sequences may be used in a method of performing highly efficient gene insertion or gene replacement. The variant FRT sequences each undergo a recombination reaction with another variant FRT of the same sequence in the presence of recombinase FLP. The method is useful for producing transgenic animal cells and animals. By locally inserting the DNA and recombinase FLP, genes can be targeted to specific

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 10:58:49 ; Search time 741.75 Seconds
(without alignments)
2221.068 Million cell updates/sec

Title: US-10-089-380-2

Perfect score: 34

Sequence: 1 gaggttctactctctgagaataggaaattc 34

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	34	6	BD013285
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3	34	100.0	52	6	BD013310
4	32.4	95.3	34	6	BD013288
5	32.4	95.3	52	6	BD013298
6	32.4	95.3	52	6	BD013307
7	30.8	90.6	34	6	A59775
8	30.8	90.6	34	6	AR067801
9	30.8	90.6	34	6	AR105498
10	30.8	90.6	34	6	AR130339
11	30.8	90.6	34	6	AR142481
12	30.8	90.6	34	6	BD246903
13	30.8	90.6	34	6	BD267670
14	30.8	90.6	34	6	C0813068
15	30.8	90.6	34	6	E43464
16	30.8	90.6	34	6	I59685
17	30.8	90.6	34	6	I69353
18	30.8	90.6	34	6	AR194975
19	30.8	90.6	34	6	AR232395

C 20	30.8	90.6	34	6	AR234678	Sequence
C 21	30.8	90.6	34	6	AR264370	Sequence
C 22	30.8	90.6	34	6	AR302446	Sequence
C 23	30.8	90.6	34	6	AR302544	Sequence
C 24	30.8	90.6	34	6	AR307970	Sequence
C 25	30.8	90.6	34	6	AR342117	Sequence
C 26	30.8	90.6	34	6	AR370679	Sequence
C 27	30.8	90.6	34	6	AR403690	Sequence
C 28	30.8	90.6	34	6	AR438854	Sequence
C 29	30.8	90.6	34	6	AR477307	Sequence
C 30	30.8	90.6	34	6	AR494802	Sequence
C 31	30.8	90.6	34	6	AR527595	Sequence
C 32	30.8	90.6	34	6	AX101007	Sequence
C 33	30.8	90.6	34	6	AX269147	Sequence
C 34	30.8	90.6	34	6	AX359678	Sequence
C 35	30.8	90.6	34	6	AX453121	Sequence
C 36	30.8	90.6	34	6	AX555208	Sequence
C 37	30.8	90.6	34	6	AX657059	Sequence
C 38	30.8	90.6	34	6	AX657060	Sequence
C 39	30.8	90.6	34	6	BD013284	DNA compr
C 40	30.8	90.6	34	6	BD013286	DNA compr
C 41	30.8	90.6	34	6	BD013287	DNA compr
C 42	30.8	90.6	34	6	BD083074	Antisense
C 43	30.8	90.6	34	6	BD093613	Antisense
C 44	30.8	90.6	34	6	BD094631	Method fo
C 45	30.8	90.6	35	6	BD271118	Methods f

ALIGNMENTS

BD013285 34 bp DNA linear PAT 02-AUG-2002
DNA comprising mutant FRT sequence.

BD013285.1 GI:22093474

KEYWORDS WO 0123545-A/2.

Saccharomyces cerevisiae (baker's yeast)

Saccharomyces cerevisiae

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

1 (bases 1 to 34)

Saito, I. and Kanegae, Y.

DNA comprising mutant FRT sequence

Patent: WO 0123545-A 2 05-APR-2001;

IZUMU SAITO, YUMI KANEGAE

OS Saccharomycetes cerevisiae (yeast)

PN WO 0123545-A/2

PD 05-APR-2001

PF 28-SEP-2000 WO 2000JP006686

PR 30-SEP-1999 JP 99P 280210, 06-DEC-1999 JP 99P 346727 P1

PC C12N15/11, C12N15/10, A01K67/027, A61K48/00

CC DNA comprising mutant FRT sequence

EH Key Location/Qualifiers

FT source 1..34

FT Location/Qualifiers

/organism='Saccharomyces cerevisiae'

/mol_type='genomic DNA'

/db_xref='taxon:4932'

ORIGIN

Query Match 100.0%; Score 34; DB 6; Length 34;

Best Local Similarity 100.0%; Pred. No. 0.00015;

Mismatches 0; Indels 0; Gaps 0;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAAGTTCTTACTCTCTGAGAATAGGAATTC 34

|||||

1 GAAGTTCTTACTCTCTGAGAATAGGAATTC 34

|||||

Qy

Db